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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/634,287A

DATE: 08/02/2002

TIME: 09:00:02

Input Set : A:\sequence\_DM6909B.txt.txt

Output Set: N:\CRF3\08022002\I634287A.raw

P.6

4 <110> APPLICANT: Bristol-Myers Squibb Company  
 6 <120> TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES  
 8 <130> FILE REFERENCE: DM6909B  
 10 <140> CURRENT APPLICATION NUMBER: US/09/634,287A  
 12 <141> CURRENT FILING DATE: 2000-08-09  
 14 <160> NUMBER OF SEQ ID NOS: 21  
 16 <170> SOFTWARE: PatentIn version 3.0  
 18 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 4192  
 22 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (406)..(2916)  
 32 <400> SEQUENCE: 1

ENTERED

33	acagacacat atgcacgaga gagacagagg aggaaagaga cagagacaaa ggcacagcgg	60
35	aagaaggcag agacaggcgca ggcacagaag cggcccgac agagtcctac agagggagag	120
37	gccagagaag ctgcagaaga cacaggcagg gagagacaaa gatccagggaa aggagggctc	180
39	aggaggagag tttggagaag ccagaccctt gggcacctct cccaaagccca aggactaagt	240
41	tttctccatt tccttaacg gtcctcagcc cttctaaaaa ctttgcctct gaccttggca	300
43	ggagtccaag cccccaggct acagagagga gctttccaaa gctagggtgt ggaggacttg	360
45	gtgcctaga cggcctcagt ccctcccagc tgcagtagcca gtgcc atg tcc cag aca	417
46	Met Ser Gln Thr	
47	1	
49	ggc tcg cat ccc ggg agg ggc ttg gca ggg cgc tgg ctg tgg gga gcc	465
50	Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp Leu Trp Gly Ala	
51	5 10 15 20	
53	caa ccc tgc ctc ctc ccc att gtg ccg ctc tcc tgg ctg gtg tgg	513
54	Gln Pro Cys Leu Leu Pro Ile Val Pro Leu Ser Trp Leu Val Trp	
55	25 30 35	
57	ctg ctt ctg cta ctg ctg gcc tct ctc ctg ccc tca gcc ccg ctg gcc	561
58	Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser Ala Arg Leu Ala	
59	40 45 50	
61	agc ccc ctc ccc cgg gag gag gag atc gtg ttt cca gag aag ctc aac	609
62	Ser Pro Leu Pro Arg Glu Glu Ile Val Phe Pro Glu Lys Leu Asn	
63	55 60 65	
65	ggc agc gtc ctg cct ggc tcg ggc gcc cct gcc agg ctg ttg tgc cgc	657
66	Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg Leu Leu Cys Arg	
67	70 75 80	
69	ttg cag gcc ttt ggg gag acg ctg cta cta gag ctg gag cag gac tcc	705
70	Leu Gln Ala Phe Gly Glu Thr Leu Leu Glu Leu Glu Gln Asp Ser	
71	85 90 95 100	
73	ggt gtg cag gtc gag ggg ctg aca gtg cag tac ctg ggc cag gcg cct	753

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**Output Set: N:\CRF3\08022002\I634287A.raw**

74 Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro			
75 105	110	115	
77 gag ctg ctg ggt gga gca gag cct ggc acc tac ctg act ggc acc atc		801	
78 Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile			
79 120	125	130	
81 aat gga gat ccg gag tcg gtg gca tct ctg cac tgg gat ggg gga gcc		849	
82 Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala			
83 135	140	145	
85 ctg tta ggc gtg tta caa tat cgg ggg gct gaa ctc cac ctc cag ccc		897	
86 Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro			
87 150	155	160	
89 ctg gag gga ggc acc cct aac tct gct ggg gga cct ggg gct cac atc		945	
90 Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile			
91 165	170	175	180
93 cta cgc cgg aag agt cct gcc agc ggt caa ggt ccc atg tgc aac gtc		993	
94 Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn Val			
95 185	190	195	
97 aag gct cct ctt gga agc ccc agc ccc aga ccc cga aga gcc aag cgc		1041	
98 Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala Lys Arg			
99 200	205	210	
101 ttt gct tca ctg agt aga ttt gtg gag aca ctg gtg gtg gca gat gac		1089	
102 Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val Ala Asp Asp			
103 215	220	225	
105 aag atg gcc gca ttc cac ggt gcg ggg cta aag cgc tac ctg cta aca		1137	
106 Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg Tyr Leu Leu Thr			
107 230	235	240	
109 gtg atg gca gca gca gcc aag gcc ttc aag cac cca agc atc cgc aat		1185	
110 Val Met Ala Ala Ala Lys Ala Phe Lys His Pro Ser Ile Arg Asn			
111 245	250	255	260
113 cct gtc agc ttg gtg gtg act cgg cta gtg atc ctg ggg tca ggc gag		1233	
114 Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu Gly Ser Gly Glu			
115 265	270	275	
117 gag ggg ccc caa gtg ggg ccc agt gct gcc cag acc ctg cgc agc ttc		1281	
118 Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr Leu Arg Ser Phe			
119 280	285	290	
121 tgt gcc tgg cag cgg ggc ctc aac acc cct gag gac tgc gac cct gac		1329	
122 Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp Ser Asp Pro Asp			
123 295	300	305	
125 cac ttt gac aca gcc att ctg ttt acc cgt cag gac ctg tgt gga gtc		1377	
126 His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Val			
127 310	315	320	
129 tcc act tgc gac acg ctg ggt atg gct gat gtg ggc acc gtc tgt gac		1425	
130 Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp			
131 325	330	335	340
133 ccg gct cgg agc tgt gcc att gtg gag gat gat ggg ctc cag tca gcc		1473	
134 Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala			
135 345	350	355	
137 ttc act gct gct cat gaa ctg ggt cat gtc ttc aac atg ctc cat gac		1521	
138 Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn Met Leu His Asp			

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139	360	365	370	
141	aac tcc aag cca tgc atc agt ttg aat ggg cct ttg agc acc tct cgc			1569
142	Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg			
143	375	380	385	
145	cat gtc atg gcc cct gtg atg gct cat gtg gat cct gag gag ccc tgg			1617
146	His Val Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp			
147	390	395	400	
149	tcc ccc tgc agt gcc cgc ttc atc act gac ttc ctg gac aat ggc tat			1665
150	Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr			
151	405	410	415	420
153	ggg cac tgt ctc tta gac aaa cca gag gct cca ttg cat ctg cct gtg			1713
154	Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro Val			
155	425	430	435	
157	act ttc cct ggc aag gac tat gat gct gac cgc cag tgc cag ctg acc			1761
158	Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln Leu Thr			
159	440	445	450	
161	ttc ggg ccc gac tca cgc cat tgt cca cag ctg ccg ccc tgt gct			1809
162	Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro Pro Cys Ala			
163	455	460	465	
165	gcc ctc tgg tgc tct ggc cac ctc aat ggc cat gcc atg tgc cag acc			1857
166	Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala Met Cys Gln Thr			
167	470	475	480	
169	aaa cac tcg ccc tgg gcc gat ggc aca ccc tgc ggg ccc gca cag gcc			1905
170	Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys Gly Pro Ala Gln Ala			
171	485	490	495	500
173	tgc atg ggt ggt cgc tgc ctc cac atg gac cag ctc cag gac ttc aat			1953
174	Cys Met Gly Gly Arg Cys Leu His Met Asp Gln Leu Gln Asp Phe Asn			
175	505	510	515	
177	att cca cag gct ggt ggc tgg ggt cct tgg gga cca tgg ggt gac tgc			2001
178	Ile Pro Gln Ala Gly Gly Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys			
179	520	525	530	
181	tct cgg acc tgt ggg ggt ggt gtc cag ttc tcc cga gac tgc acg			2049
182	Ser Arg Thr Cys Gly Gly Val Gln Phe Ser Ser Arg Asp Cys Thr			
183	535	540	545	
185	agg cct gtc ccc cgg aat ggt ggc aag tac tgt gag ggc cgc cgt acc			2097
186	Arg Pro Val Pro Arg Asn Gly Gly Lys Tyr Cys Glu Gly Arg Arg Thr			
187	550	555	560	
189	cgc ttc cgc tcc tgc aac act gag gac tgc cca act ggc tca gcc ctg			2145
190	Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu			
191	565	570	575	580
193	acc ttc cgc gag gag cag tgt gct gcc tac aac cac cgc acc gac ctc			2193
194	Thr Phe Arg Glu Glu Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu			
195	585	590	595	
197	ttc aag agc ttc cca ggg ccc atg gac tgg gtt cct cgc tac aca ggc			2241
198	Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly			
199	600	605	610	
201	gtg gcc ccc cag gac cag tgc aaa ctc acc tgc cag gcc cgg gca ctg			2289
202	Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu			
203	615	620	625	

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205 ggc tac tac tat gtg ctg gag cca cggtgt gta gat ggg acc ccc tgt	2337
206 Gly Tyr Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys	
207 630 635 640	
209 tcc ccg gac agc tcc tcg gtc tgt gtc cag ggc cga tgc atc cat gct	2385
210 Ser Pro Asp Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	
211 645 650 655 660	
213 ggc tgt gat cgc atc att ggc tcc aag aag ttt gac aag tgc atg	2433
214 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Phe Asp Lys Cys Met	
215 665 670 675	
217 gtg tgc gga ggg gac ggt tct ggt tgc agc aag cag tca ggc tcc ttc	2481
218 Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly Ser Phe	
219 680 685 690	
221 agg aaa ttc agg tac gga tac aac aat gtg gtc act atc ccc gcg ggg	2529
222 Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile Pro Ala Gly	
223 695 700 705	
225 gcc acc cac att ctt gtc cgg cag cag gga aac cct ggc cac cgg agc	2577
226 Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro Gly His Arg Ser	
227 710 715 720	
229 atc tac ttg gcc ctg aag ctg cca gat ggc tcc tat gcc ctc aat ggt	2625
230 Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser Tyr Ala Leu Asn Gly	
231 725 730 735 740	
233 gaa tac acg ctg atg ccc tcc aca gat gtg gta ctg cct ggg gca	2673
234 Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp Val Val Leu Pro Gly Ala	
235 745 750 755	
237 gtc agc ttg cgc tac agc ggg gcc act gca gcc tca gag aca ctg tca	2721
238 Val Ser Leu Arg Tyr Ser Gly Ala Thr Ala Ala Ser Glu Thr Leu Ser	
239 760 765 770	
241 ggc cat ggg cca ctg gcc cag cct ttg aca ctg caa gtc cta gtg gct	2769
242 Gly His Gly Pro Leu Ala Gln Pro Leu Thr Leu Gln Val Leu Val Ala	
243 775 780 785	
245 ggc aac ccc cag gac aca cgc ctc cga tac agc ttc ttc gtg ccc cgg	2817
246 Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe Phe Val Pro Arg	
247 790 795 800	
249 ccg acc cct tca acg cca cgc ccc act ccc cag gac tgg ctg cac cga	2865
250 Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp Trp Leu His Arg	
251 805 810 815 820	
253 aga gca cag att ctg gag atc ctt cgg cgg cgc ccc tgg gcg ggc agg	2913
254 Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Pro Trp Ala Gly Arg	
255 825 830 835	
257 aaa taacctcaact atccccggctg ccctttctgg gcaccggggc ctccggactta	2966
258 Lys	
261 gctggggagaaa agagagagct tctgttgctg cctcatgcta agactcagtg gggaggggct	3026
263 gtggggcgtga gacctgcccc tcctctctgc cctaattgcgc aggctggccc tgccctgggtt	3086
265 tcctgccctg ggagggcagtg atgggttagt ggatggaaagg ggctgacaga cagccctcca	3146
267 tctaaactgc cccctctgcc ctgcgggtca caggaggag gggaaaggca gggagggcct	3206
269 gggcccccagt tgtattttat tagtatttat tcactttat ttagcaccag ggaaggggac	3266
271 aaggactagg gtcctgggaa acctgaccnc tgaccctca tagccctcac cctggggcta	3326
273 gggaaatccag ggtgggtgt ataggtataa gtgggtgtgt tatgcgtgtg tgtgtgtgt	3386
275 tggaaatgtg tgtgtgctta tgtatgaggt acaacctgtt ctgtttctt cttccctgaat	3446

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277	tttatttttt	gggaaaagaa	aagtcaaggg	taggtggc	cttcagggag	tgagggatta	3506
279	tcctttttt	tttcttcctt	tctttctttt	tttttttag	acagaatctc	gctctgtcgc	3566
281	ccaggctgga	gtgcaatggc	acaatctcg	ctcaactgcat	cctccgcctc	ccgggttcaa	3626
283	gtgattctca	tgcctcagcc	tcctgagtag	ctgggattac	aggctctgc	caccacgccc	3686
285	ggctaatttt	tgtttgttt	tgtttggaga	cagagtctcg	ctattgtcac	cagggctgga	3746
287	atgatttcag	ctcaactgcaa	ctttcgcac	ctggggttcca	gcaattctcc	tgccctcagcc	3806
289	tcccgagtag	ctgagattat	aggcacctac	caccacgccc	ggctaatttt	tgtatttta	3866
291	gtagagacgg	ggtttccacca	tgttggccag	gctggtctcg	aactcctgac	cttaggtgat	3926
293	ccactcgcct	tcatctccca	aagtgctggg	attacaggcg	tgagccacccg	tgccctggcca	3986
295	cgcggcaacta	attttgtat	ttttagtaga	gacagggtt	caccatgtt	gccaggctgc	4046
297	tcttgaactc	ctgacccctag	gtaatcgacc	tgcctcggcc	tcccaaagt	ctgggattac	4106
299	aggtgtgagc	caccacgccc	ggtacatatt	ttttaaattt	aattctacta	tttatgtgat	4166
301	ccttttggag	tcagacagat	gtgggt				4192
303	<210>	SEQ ID NO:	2				
305	<211>	LENGTH:	837				
307	<212>	TYPE:	PRT				
309	<213>	ORGANISM:	Homo sapiens				
311	<400>	SEQUENCE:	2				
313	Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp						
314	1	5	10	15			
316	Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser						
317	317	20	25	30			
319	Trp Leu Val Trp Leu Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser						
320	319	35	40	45			
322	Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro						
323	322	50	55	60			
325	Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg						
326	325	65	70	75	80		
328	Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu						
329	328	85	90	95			
331	Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu						
332	331	100	105	110			
334	Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu						
335	334	115	120	125			
337	Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp						
338	337	130	135	140			
340	Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu						
341	340	145	150	155	160		
343	His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro						
344	343	165	170	175			
346	Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro						
347	346	180	185	190			
349	Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg						
350	349	195	200	205			
352	Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val						
353	352	210	215	220			
355	Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg						
356	355	225	230	235	240		
358	Tyr Leu Leu Thr Val Met Ala Ala Ala Lys Ala Phe Lys His Pro						

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 12

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:21